

CS -- Column material: 10 μ M Lichrosphere® 100 RP-18 column from Merck Darmstadt GmbH; 250 x4 --

[Please replace page 14, line 36 with the following:]

-- Mass spectrometry: calculated mass MH_2^{2+} : 1436.2 g/mol
found mass MH_2^{2+} : 1436.4 g/mol --

Please delete lines 5-6 on page 15.

Please replace the text on page 17, lines 5 with the following:

C -- What is claimed is: --

In the Claims

Please cancel claims 4-7, 22-23, and 32.

Please amend claims 1-3, 8-21, and 24-31 as follows.

Please add new claims 33-64.

1. A recognition system comprising:

C6 (a) at least one immobilized capture sequence having at least one binding site for a complementary recognition sequence, wherein the capture sequence is selected from the group consisting of pyranosyl nucleic acid (p-NA) and nucleic acid having one or more aminocyclohexylethanoic acid (CNA) units; and

(b) at least one complementary recognition sequence that binds to the capture sequence and contains at least one binding site for a substrate S, wherein the recognition sequence is selected from the group consisting of pyranosyl nucleic acid (p-NA) and nucleic acid having one or more aminocyclohexylethanoic acid (CNA) units, and wherein the binding of the capture sequence to the recognition sequence forms a molecular pairing system.

2. The recognition system according to Claim 1, wherein the molecular pairing system is a complex that is formed by association of the capture sequence with the complementary recognition sequence via non-covalent interactions.

C6 3. The recognition system according to Claim 2, wherein the non-covalent interactions are selected from the group consisting of hydrogen bridges, salt bridges, stacking, metal ligands, charge-transfer complexes, and hydrophobic interactions.

C7 8. The recognition system according to claim 1, wherein at least one nucleobase of the capture or recognition sequences is selected from the group consisting of purine, 2,6-diaminopurine, 6-purinethiol, pyridine, pyrimidine, adenine, guanine, isoguanine, 6-thioguanine, xanthine, hypoxanthine, thymine, cytosine, isocytosine, indole, tryptamine, N-phthaloyltryptamine, uracil, caffeine, theobromine, theophylline, benzotriazole, and acridine.

9. The recognition system according to claim 1, wherein the p-NA is selected from the group consisting of ribopyranosyladenosine, ribopyranosylguanosine,

ribopyranosylthymidine, ribopyranosylcytosine, ribopyranosyltryptamine or ribopyranosyl-N-phthalotryptamine, ribopyranosyluracil, and their 2-amino-4-(carboxymethyl)ribopyranosyl derivatives.

10. The recognition system according to claim 1, wherein the length of the capture or recognition sequences are at least about 4-50 nucleotides.

11. The recognition system according to claim 1, wherein the capture sequence is immobilized on a carrier.

12. The recognition system according to Claim 11, wherein the carrier is selected from the group consisting of ceramic, metal, glasses, polymers, and crystalline materials.

13. The recognition system according to Claim 11, wherein the capture sequence is immobilized on the carrier by means of a covalent bond, quasi-covalent bond or supramolecular bond by association of two or more molecular species.

14. The recognition system according to claim 11, wherein the capture sequence is immobilized at defined sites of the carrier.

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15. The recognition system according to Claim 14, wherein the defined sites of the carrier are addressed.

16. The recognition system according to claim 11, wherein the capture sequence is immobilized on a carrier electrode of the carrier.

17. The recognition system according to claim 1, wherein the binding site is a biomolecule that binds substrate S.

18. The recognition system according to Claim 17, wherein the biomolecule is selected from peptides, peptoids, proteins, lipids, glycoproteins, filament constituents, viruses, viroids, saccharides, nucleic acids, and their active moieties.

19. The recognition system according to claim 1, wherein the immobilized capture sequence contains various binding sites for the complementary recognition sequence, by means of which various complementary recognition sequences binds to the capture sequence.

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20. The recognition system according to claim 1, wherein at least one further complementary recognition sequence is bound to the capture sequence.

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24. The recognition system according to claim 34, wherein the various biomolecules bind the substrate S.

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26. The recognition system according to claim 1, wherein the at least one binding site for substrate S comprises antibodies, antibody fragments, and derivatives thereof.

27. A process for identifying a substrate S in a sample, the process comprising:
- (a) providing a recognition system comprising:
 - at least one immobilized capture sequence having at least one binding site for a complementary recognition sequence, wherein the capture sequence is selected from the group consisting of pyranosyl nucleic acid (p-NA) and nucleic acid having one or more aminocyclohexylethanoic acid (CNA) units; and
 - at least one complementary recognition sequence that binds to the capture sequence and contains at least one binding site for a substrate S, wherein the recognition sequence is selected from the group consisting of pyranosyl nucleic acid (p-NA) and nucleic acid having one or more aminocyclohexylethanoic acid (CNA) units, and wherein the binding of the capture sequence to the recognition sequence forms a molecular pairing system;
 - (b) contacting the recognition sequence containing at least one binding site for substrate S with a sample containing substrate S;
 - (c) simultaneously or successively contacting the recognition sequence and sample with the immobilized capture sequence to form an immobilized complex; and
 - (d) detecting a complex of immobilized capture sequence, recognition sequence, and substrate S.

28. The process according to Claim 27, wherein the formation of the complex is controlled by means of physical parameters.

29. The process according to Claim 27, wherein the complex is detected by means of a label on the complex or by directly detecting the complex itself.

30. The process according to claim 27, further comprising isolating the complex of the recognition sequence and substrate S.

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31. The process according to Claim 27, wherein the complex of recognition sequence and substrate S is in a binding equilibrium, and further comprising isolating the complex after freezing the binding equilibrium.

33. The process according to claim 30, further comprising the step of covalently cross-linking the recognition sequence and substrate S.

34. The recognition system according to claim 20, wherein the binding site of at least one further complementary recognition sequence is an additional biomolecule.

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35. The recognition system according to claim 1, wherein the length of the capture or recognition sequences is at least about 4-25 nucleotides.

36. The recognition system according to claim 1, wherein the length of the capture or recognition sequences is at least about 4-15 nucleotides.

37. The recognition system according to claim 1, wherein the length of the capture or recognition sequences is at least about 4-10 nucleotides.

38. The recognition system according to Claim 11, wherein the carrier comprises a noble metal.

39. The recognition system according to Claim 11, wherein the carrier comprises a (bio)molecule polymer.

40. The recognition system according to Claim 11, wherein the carrier comprises a structural protein.

41. The recognition system according to Claim 13, wherein the two or more molecular species are selected from a group consisting of peptides, peptoids, proteins, linear oligo- or polysaccharides, nucleic acids, heterocycles, branched oligo- or polysaccharides, antibodies, and derivatives thereof.

42. The recognition system according to Claim 1, wherein the p-NA is a pyranosyl-RNA (p-RNA).

43. The recognition system according to claim 11, wherein the capture sequence is immobilized at defined sites of the carrier in a matrix.

44. The process of claim 28, wherein the physical parameters are selected from the group consisting of temperature, salts, solvents, and electrophoretic processes.

45. The process according to Claim 29, wherein the complex is detected by means of radioactive labeling, fluorescent labeling, enzymatic labeling, redox labeling, spin labeling of the recognition sequence, redox processes in an environment or on an electrode, impedance measurement, or direct current measurement.

46. A recognition system comprising:

at least one immobilized capture sequence that is synthetic and does not bind to naturally occurring nucleic acids; and

at least one complementary recognition sequence that binds to the capture sequence and contains at least one binding site for a substrate S, wherein the recognition sequence is synthetic and does not bind to naturally occurring nucleic acids, wherein the binding of the recognition sequence to the capture sequence forms a non-covalent, hydrogen-bonded molecular pairing system.

47. The recognition sequence of claim 46, wherein the capture and/or recognition sequences are selected from the group consisting of pyranosyl nucleic acid (p-NA) and nucleic acid having one or more aminocyclohexylethanoic acid (CNA) units.

48. The recognition sequence of claim 47, wherein the p-NA is a pyranosyl RNA (p-RNA).

49. The recognition sequence of claim 46, wherein the binding site is a biomolecule that binds substrate S.

50. The recognition sequence of claim 49, wherein the biomolecule is selected from peptides, peptoids, proteins, lipids, glycoproteins, filament constituents, viruses, viroids, antibodies, antibody fragments, saccharides, and nucleic acids, and their active moieties,

51. The recognition system according to claim 47, wherein the p-NA is selected from the group consisting of ribopyranosyladenosine, ribopyranosylguanosine, ribopyranosylthymidine, ribopyranosylcytosine, ribopyranosyltryptamine or ribopyranosyl-N-phthalotryptamine, ribopyranosyluracil, and their 2-amino-4-(carboxymethyl)ribopyranosyl derivatives.

52. The recognition system according to claim 46, wherein the capture sequence is immobilized on a carrier.

53. The recognition system according to claim 52, wherein the capture sequence is immobilized at defined sites of the carrier.

54. The recognition system according to claim 52, wherein the capture sequence is immobilized on a carrier electrode of the carrier.

55. The recognition system according to claim 46, wherein the immobilized capture sequence contains various binding sites for the complementary recognition sequence, by means of which various complementary recognition sequences binds to the capture sequence.

56. The recognition system according to claim 55, wherein at least one further complementary recognition sequence is bound to the capture sequence, wherein the binding site of at least one further complementary recognition sequence is an additional biomolecule that binds the substrate S.

57. A process for identifying a substrate S in a sample, the process comprising:

(a) providing a recognition system comprising:

at least one immobilized capture sequence that is synthetic and does not bind to naturally occurring nucleic acids; and

at least one complementary recognition sequence that binds to the capture sequence and contains at least one binding site for a substrate S, wherein the recognition sequence is synthetic and does not bind to naturally occurring nucleic acids, wherein the binding of the recognition sequence to the capture sequence forms a non-covalent, hydrogen-bonded molecular pairing system.

(b) contacting the recognition sequence containing at least one binding site for substrate S with a sample containing substrate S;

(c) simultaneously or successively contacting the recognition sequence and sample with the immobilized capture sequence to form an immobilized complex; and

(d) detecting a complex of immobilized capture sequence, recognition sequence, and substrate S.

58. The process according to claim 57, wherein the formation of the complex is controlled by means of physical parameters.

59. The process according to claim 58, wherein the physical parameters are selected from the group consisting of temperature, salts, solvents, and electrophoretic processes.

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60. The process according to claim 57, wherein the complex is detected by means of a label on the complex or by directly detecting the complex itself.

61. The process according to claim 60, wherein the complex is detected by means of radioactive labeling, fluorescent labeling, enzymatic labeling, redox labeling, spin labeling of the recognition sequence, redox processes in an environment or on an electrode, impedance measurement, or direct current measurement.

62. The process according to claim 57, further comprising isolating the complex of the recognition sequence and substrate S.

63. The process according to claim 57, wherein the complex of the recognition sequence and substrate S is in a binding equilibrium, and further comprising isolating the complex after freezing the binding equilibrium.

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64. The process according to claim 62, further comprising the step of covalently cross-linking the recognition sequence and substrate S.
